Fig.1

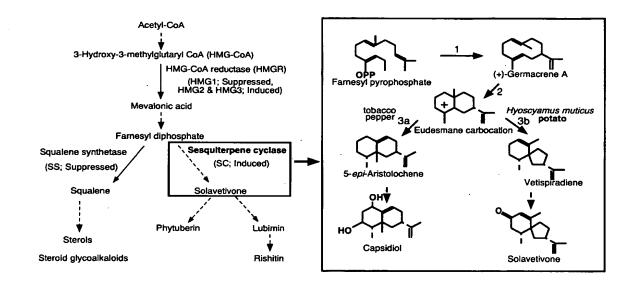
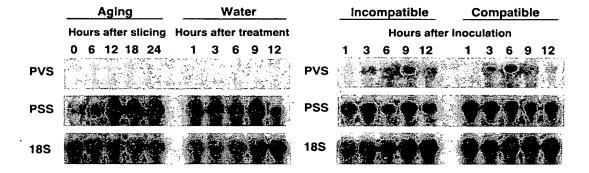


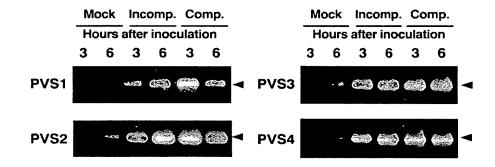
Fig.2



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Fig.3



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Fig.4

| Mock | | | | | | | Incomp. | | | | | | Comp. | | | | | | | | |
|------|---|---|---|-----|----|----|---------|-----|-----|-------|-----|-------|-------|---|---|---|---|---|----|----|---|
| | | | | | | | Но | urs | aft | er ir | 100 | ulati | ion | | | | | | | | |
| 0 | 1 | 3 | 6 | 9 | 12 | 24 | 0 | 1 | 3 | 6 | 9 | 12 | 24 | 0 | 1 | 3 | 6 | 9 | 12 | 24 | |
| | | | | ٠., | | | | | | | | | | | | | | | • | | *************************************** |

Fig.5

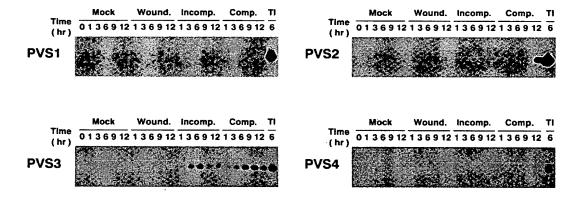


Fig. 6

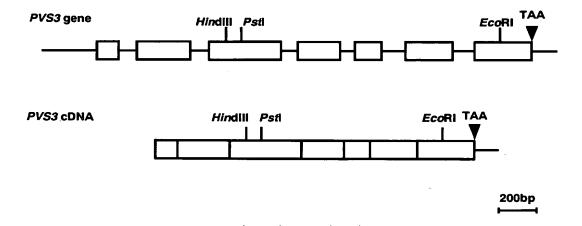
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Fig. 7

| 773 198 | CCTTGAGCAGTCTCTCCATAAGAGCATTCCAAGAGTCGAGACGCGCTACTTCATCTCC L E Q S L B K S I P R V E T R Y F I S | AT 832 I 217 |
|------------|--|------------------|
| 833 218 | CTACGAAGAGGAGGAATTTAAGAATGATGTGTTGCTTCGATTTGCCAAATTGGATTAC Y E E E F K N D V L L R F A K L D Y | AA 892 N 237 |
| 893 238 | CTTACTCCAGATGTTGCACAAACACGAACTTAGTGAAGTATCAAGgtatacagatgtg L L Q M L H K H E L S E V S R | 252 252 |
| | aagttgaattaaaaatactagtataaattatttgttgatagtaatttctaagattggt | |
| 253 | | D 268 |
| 073 269 | R A V E C Y P W T M G V Y A E P Q Y S | AG 1132 Q 288 |
| 133 289 | G GCTCGTGTCATCCTTGCAAAGACTATAGCAATGATTTCGATAGTAGATGACACATTCG O A R V I L A R T I A M I S I V D D T F | AT 1192 D 308 |
| 193 309 | GCTTATGGAATAGTAAAGAACTTGAGGTCTACACCGATGCCATACAAAGgtatggac A Y G I V K E L E V Y T D A I Q R | 1252 325 |
| 253 | gcctctccaacagttcatggatttattagacgggaaacttactaaatctctttctgtt | tt 1312 |
| 313 | attagGTGGGATATTAGTCAAATTGATCGACTCCCAGAATACATGAAAGTTAGTT | |
| 326 | | K 343 |
| | | AT 1432 |
| 344 | GCTCTTTTGGATCTCTATGAAGATTATGAAAAGGAGTTGTCAAAGGATGGCAGATCCG A L L D L Y E D Y E K E L S K D G R S | D 363 |
| | | ta 1492 |
| 364 | B GTTGTCCACTACGCAAAAGAAAGAgtaggactcactgatttctatttaaaaacacttg V V B Y A R E R | 371 |
| 403 | | tg 1552 |
| EE2 | l tttaccttatactatttctttattatacaattagatctgttatgggagtattgatggt l aatgtcttgtggtttctgttaaacagATGAAGGAGATTGTGAGAAACTATTTTGTAGA | AG 1612 |
| 372 | M K E I V R N Y F V E | 382 |
| 612 | CAAAGTGGTTCATTGAGGGATATATGCCGCCTGTTTCTGAGTATCTTAGCAATGCATT | AG 1672 |
| | AKWFIEGYMPPVSEYLSNAL | 402 |
| 673 | CTACCAGCACATATTACTTGCTAACTACAACATCCTATTTGGGAGTGAAGTCAGCAAC | AA 1732 |
| | ATSTYYLLTTTSYLGVKSAT | |
| 733 | AGGAAGATTTTGAATGGTTGGCTACGAACCCTAAAATTCTTGAAGCCAATGTGACATT | AT 1792 |
| | REDFEWLATNPKILEANVTL | 442 |
| 702 | GCCGAGTTGTTGATGACATAGCAACGTATGAGgtaattagcatcgcattacactacat | aa 1852 |
| | B C R V V D D I A T Y E | 453 |
| 853 | B atcatcttataatttagagttacagtaatttaatacaaattgatttcacatacttata | aa 1912 |
| 913 | tgaattataattgccattccagGTTGAGAAGGGTAGGGGCCAAATCGCAACAGGAATT | GA 1972 |
| 454 | VEKGRGQIATGI | E 466 |
| 973 | GTGTTATATGAGGGATTATGACGTATCAACAGAAGTAGCAATGGAAAAATTCCAAGAG | AT 2032 |
| 467 | | M 486 |
| | B GGCTGAGATAGCATGGAAGGATGTAAATGAAGGAATTCTTCGACCAACACCTGTCTCT V A E I A W K D V N E G I L R P T P V S | AC 2092 T 506 |
| 487 | | _ |
| 2093 | B AGAAATTCTTACTCGCATTCTCAATCTTGCTCGTATTATAGATGTCACTTACAAGCAC | AA 2152 |
| 507 | | N 526 |
| 2153 | TCAAGATGGATACACTCATCCCGAAAAAGTTCTAAAACCTCACATCATTGCTTTACTG | GT 2212 |
| 527 | | V 546 |
| 2213 | eta GGACTCCATTGAGATCtaaaaatttagtaaattttaatttttaaaatgttacgtaaaa eta DSIEI \star | aa 2272 551 |
| | | |
| 273 | 3 taataaaccgtaaaaataatgaagattaaggcgaacgaac | tg 2332 |
| | agaatggatgatggaaaatagatgaatatattgttatgcatgaagggtgtttcacact | |
| 393 | tttgattttgggaatgcatggacatccgcatgttgtcgactacacctcgaccaatgtt | gc 2452 |
| 453 | gcaagccacggccgatgcgggcaggccacggatgaccgttgtgtgcagtccaagggcg | at 2512 |
| 2513 | } gcggccaggccacggccgatgtcgactgaccgttgtgtgcagtccaagggcgatgcgg | gc 2572 |
| 2573 | aggecaegteegaegt | 2588 |

Fig. 8



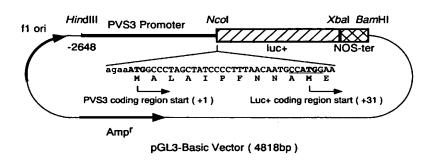
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Fig. 9

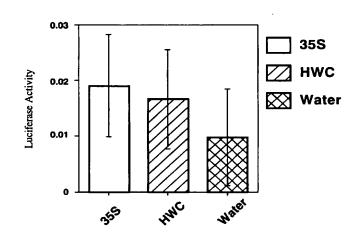
| Cyclase | | Dec | aucea Amii | no Aci | a Se | quence | 2 | | |
|-----------------------|--------------------------------|----------------|------------|----------------|--------|--------|--------------------|--|--|
| N | ıн <mark>‡</mark> | нĤ | ų. | DDXXD | | | ç coo | | |
| TEAS (N. tabacum) | 37 | 88 | 126 | 73 | 46 | 82 | 98 | | |
| | 67.5% | 60.6% Ḥ Ḥ | 77.0% H | 89.0% DXXD | 73.9% | | .8% Ç | | |
| PVS1 (S.tuberosum) | 40 | 92 | 125 | 73 | 46 | 1 | 80 | | |
| | 72.5% | 95.7% H H | 96.0% H | 100% DDXXI | | 98 | 3.9% C | | |
| PVS4 (S.tuberosum) | 33 | 92 | 125 | 73 | 46 | 1 | 80 | | |
| | 71.8% | 6 75.0% Ḥ Ḥ | 87.2% H | 98.6% DDXXI | 93.5 | % 9 | 91.1% Ç | | |
| HVS (H. muticus) | 39 | 92 | 125 | 73 | 46 | 82 | 98 | | |
| PVS3 | 76.9% | 77.4% Ḥ Ḥ | 91.2% H | 98.6% DDXXI | | 91.5% | 93.9% Ç | | |
| (S.tuberosum) | 37 | 90 | 125 | 73 | 46 | 82 | 98 | | |
| | 59.5% | 58.5% H H | 71.4% Ḥ | 78.1% DDXX | 74.5% | 79.3% | ç ^{80.6%} | | |
| PEAS (C. annuum) | 42 | 92 | 126 | 72 | 47 | 82 | 98 | | |
| | | | | comn | non do | mains | | | |
| | aristolochene specific domains | | | | | | | | |
| | ratio determinant domains | | | | | | | | |
| | vetispiradine specific domains | | | | | | | | |

Fig. 1 0

(A)

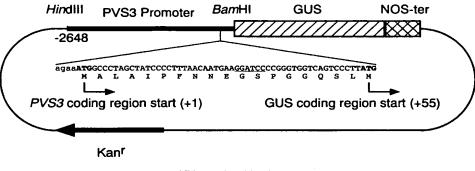


(B)



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Fig. 1 1



PBI121 (13kbp)

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Fig. 1 2

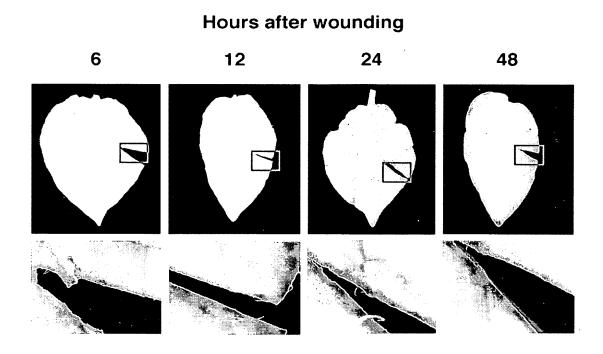


Fig. 1 3

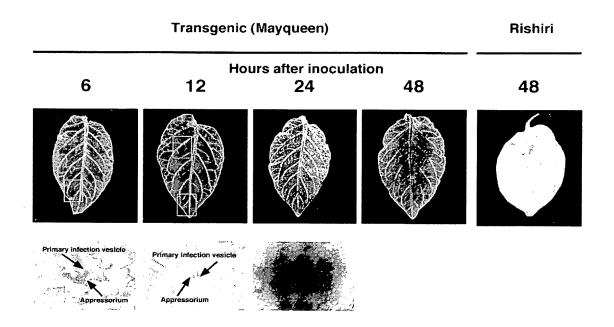


Fig. 1 4

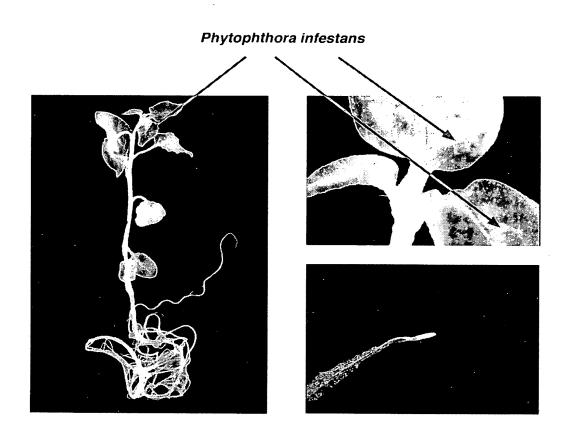
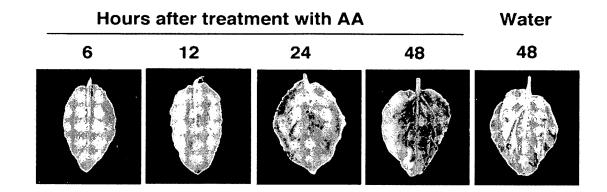


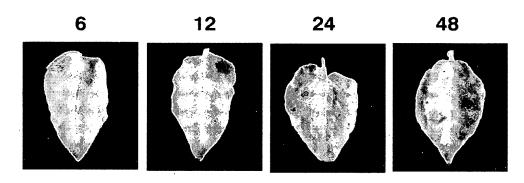
Fig. 1 5



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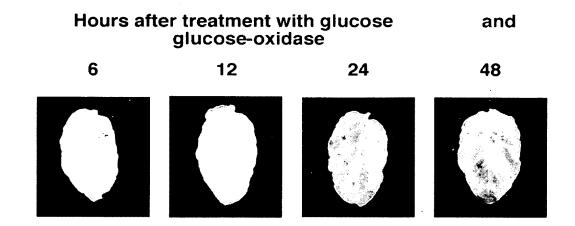
Fig. 1 6

Hours after treatment with H₂O₂



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Fig. 1 7



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Fig. 1 8

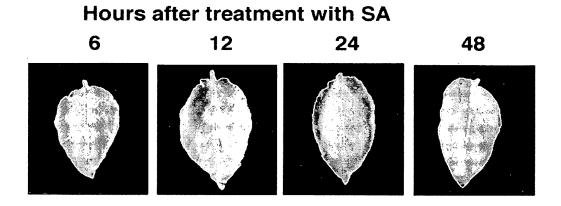
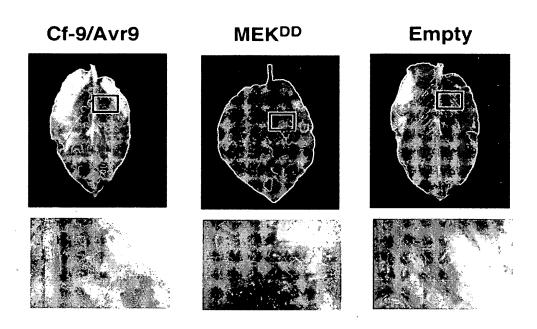


Fig. 1 9



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Fig. 2 0

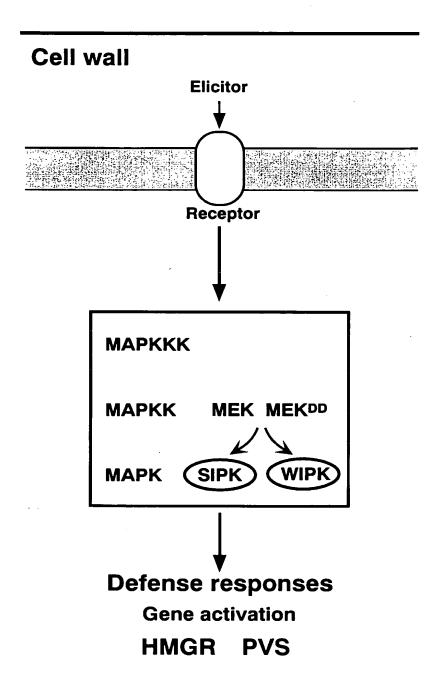


Fig. 2 1

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Fig. 2 2

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MRPLQPPPPAANSTSSAAASSMPPPSSAGQRSRPRRRTDLTLPLPQRDVALAVPLPLPPTSAPS SSSSSSSPLPTPLHFSELERVNRIGSGTGGTVYKVLHRPTGRLYALKVIYGNHEDSVRLQMCR EIEILRDVDNPNVVRCHDMFDHNGEIQVLLEFMDKGSLEGIHIPLEQPLSDLTRQVLSGLYYL HRRKIVHRDIKPSNLLINSRREVKIADFGVSRVLAQDMDPCNDSVGTIAYMSPERINTDLNHG QYDGYAGDIWSLGVSILEFYLGRFPFSVGRQGDWASLMCAICMSQPPEAPPTASREFREFIAC CLQRDPARRWTAAQLLRHPFITQNSPGTHTGPATTSLSNQAHQLLPPPPHFSSSSSS

Fig. 2 3

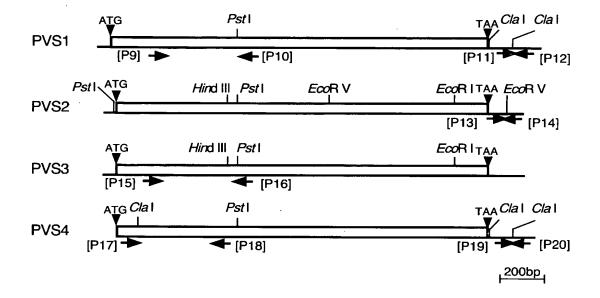


Fig. 2 4

| Name | Primer sequence |
|--------------------|--|
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| PVS3-2 (-1337) : F | 5'-CGGAATTCGTCCGCCCTTACTATTCCCATC-3' SEQ ID NO: 26 |
| PVS3-3 (-1287) : F | 5'-CGGAATTCTTTATAATAGTGCACTCATGCT-3' SEQ ID NO: 27 |
| PVS3-4 (-1237) : F | 5'-CGGAATTCGCTATATTTTTTCAAGTTGAAG-3' SEQ ID NO: 28 |
| PVS3-5 (-1187) : F | 5'-CGGAATTCGACGCCATTGAAGGAAGAAAAA-3' SEQ ID NO: 29 |
| PVS3-6 (-1137) : F | 5'-CGGAATTCACTTTCTTGGTCCCTTCGAGGC-3' SEQ ID NO: 30 |
| PVS3-7 (-1087) : F | 5'-CGGAATTCAACAAAAAAAAAGACAGACGGT-3' SEQ ID NO: 31 |
| PVS3-8 (-836) : F | 5'-CGGAATTCGTTATATAGTTTTTAAAAAAAAA3' SEQ ID NO: 32 |
| PVS3-9 (-584) : F | 5'-CGGAATTCGATTTATAACACGATGCGGGTG-3' SEQ ID NO: 33 |
| PVS3-10 (-332) : F | 5'-CGGAATTCTTACTATATATTAACTGTCCAC-3' SEQ ID NO: 34 |
| PVS3:R | 5'-CCATCGATTCCTCTTCATTGTTAAAGGGGA-3' SEQ ID NO: 35 |

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Fig. 2 5

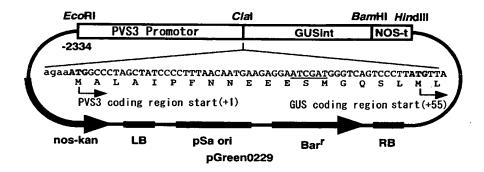
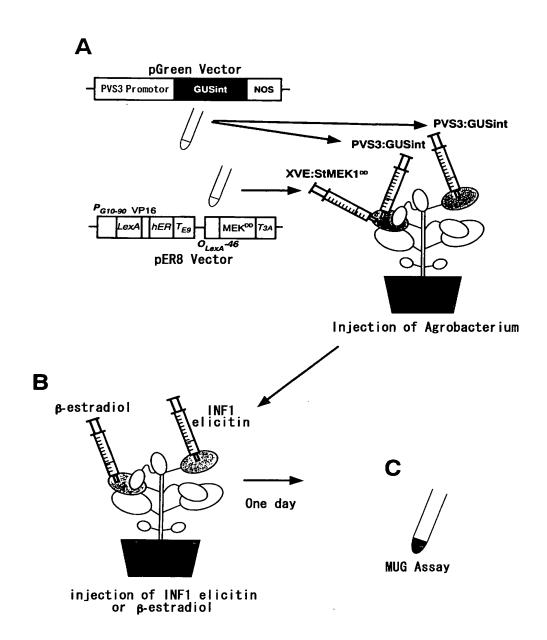


Fig. 2 6



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Fig. 2 7

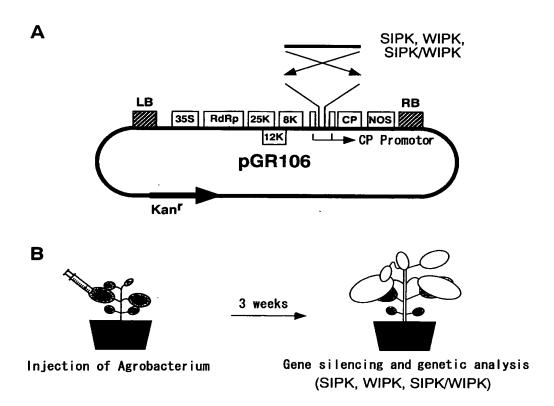
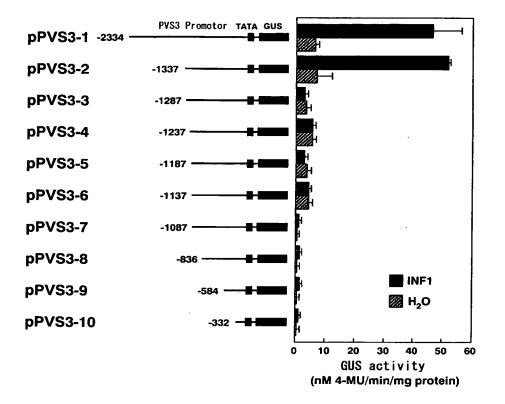


Fig. 2 8



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Fig. 29

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Fig. 3 0

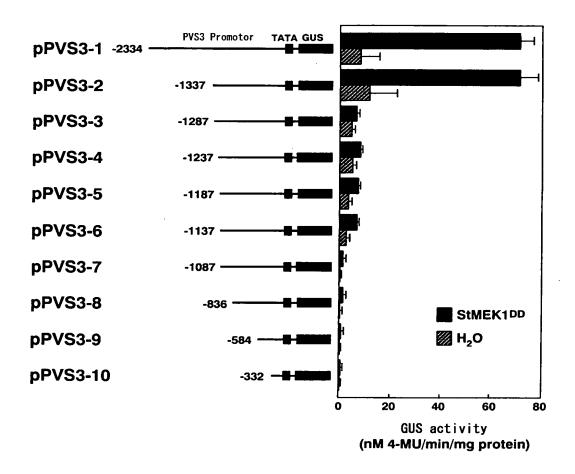


Fig. 3 1

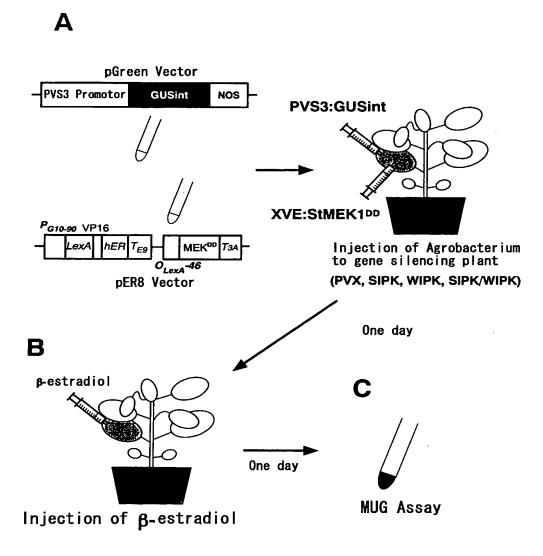
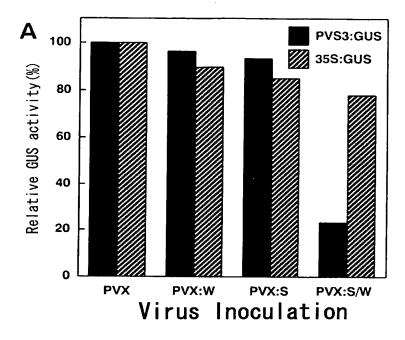
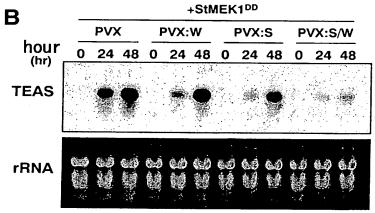


Fig. 3 2





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